

#13



PCT09

## RAW SEQUENCE LISTING

DATE: 06/04/2002

PATENT APPLICATION: US/09/856,018B

TIME: 16:04:27

Input Set : A:\BB1295 US PCT substitute sequence listing.txt

Output Set: N:\CRF3\06042002\I856018B.raw

3 <110> APPLICANT: Cahoon, Edgar B.  
 4 Kinney, Anthony J.  
 5 Cahoon, Rebecca E.  
 7 <120> TITLE OF INVENTION: Plant Diacylglycerol Acyltransferases  
 9 <130> FILE REFERENCE: BB-1295  
 11 <140> CURRENT APPLICATION NUMBER: 09/856,018B  
 12 <141> CURRENT FILING DATE: 2002-05-03  
 14 <150> PRIOR APPLICATION NUMBER: 60/110,602  
 15 <151> PRIOR FILING DATE: 1998-12-02  
 17 <150> PRIOR APPLICATION NUMBER: 60/127,111  
 18 <151> PRIOR FILING DATE: 1999-03-31  
 20 <160> NUMBER OF SEQ ID NOS: 26  
 22 <170> SOFTWARE: Microsoft Office 97  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 1888  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Arabidopsis thaliana  
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 32 gcttttcgaa atggcgattt tggattctgc tggcggtact acggtgacgg agaacgggtg 180  
 33 cggagagttc gtcgatcttg ataggcttcg tcgacggaaa tcgagatcgg attcttctaa 240  
 34 cggacttctt ctctctggtt ccgataataa ttctccttcg gatgatgttg gagctccgcg 300  
 35 cgacgttagg gatcggattg attccgttgt taacgatgac gctcaggga cagccaattt 360  
 36 ggccggagat aataacgggt gtggcgataa taacgggtgt ggaagaggcg gcggagaagg 420  
 37 aagaggaaac gccgatgcta cgtttacgta tcgaccgtcg gttccagctc atcggagggc 480  
 38 gagagagagt ccacttagct ccgacgcaat cttcaaacag agccatgccg gattattcaa 540  
 39 cctctgtgta gtagttctta ttgctgtaaa cagtagactc atcatcgaaa atcttatgaa 600  
 40 gtatgggttg ttgatcagaa cggatttctg gtttagttca agatcgctgc gagattggcc 660  
 41 gcttttcatg tgttggtat cccttcgat ctttcctttg gctgccttta cgttgagaa 720  
 42 attggtactt cagaaatata tatcagaacc tgttggtatc tttcttcata ttattatcac 780  
 43 catgacagag gttttgtatc cagtttacgt caccctaagg tgtgattctg cttttttatc 840  
 44 aggtgtcact ttgatgctcc tcacttgcat tgtgtggcta aagttgggtt cttatgctca 900  
 45 tactagctat gacataagat ccctagccaa tgcagctgat aaggccaatc ctgaagtctc 960  
 46 ctactacgtt agcttgaaga gcttggcata ttcatgggtc gctcccatat tgtgttatca 1020  
 47 gccaaagtat ccacgttctg catgtatacg gaagggttgg gtggctcgtc aatttgcaaa 1080  
 48 actggtcata ttccacggat tcatgggatt tataatagaa caatatataa atcctattgt 1140  
 49 caggaaactca aagcatcctt tgaaaggcga tcttctatat gctattgaaa gagtggtgaa 1200  
 50 gcttttcagtt ccaaatttat atgtgtggct ctgcatgttc tactgcttct tccacccttg 1260  
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 52 gaatgcaaaa agtgtgggag attactggag aatgtggaat atgcctgttc ataaatggat 1380  
 53 ggttcgacat atatacttcc cgtgcttgcg cagcaagata ccaaagacac tcgccattat 1440  
 54 cattgctttc ctagtctctg cagtctttca tgagctatgc atcgagttc cttgtcgtct 1500

ENTERED

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55 cttcaagcta tgggcttttc ttgggattat gtttcagggt cctttggtct tcatcacaaa 1560
56 ctatctacag gaaaggtttg gctcaacggt ggggaacatg atcttctggt tcatcttctg 1620
57 cattttcggg caaccgatgt gtgtgcttct ttattaccac gacctgatga accgaaaagg 1680
58 atcgatgtca tgaaacaact gttcaaaaaa tgactttctt caaacatcta tggcctcggt 1740
59 ggatctccgt tgatgtttgt gtggttctga tgctaaaacg acaaatagtg ttataaccat 1800
60 tgaagaagaa aagaaaatta gagttgttgt atctgcaaaa attttggtag agacacgcaa 1860
61 acccgtttgg attttgttat ggagtaaa 1888

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63 &lt;210&gt; SEQ ID NO: 2

64 &lt;211&gt; LENGTH: 520

65 &lt;212&gt; TYPE: PRT

66 &lt;213&gt; ORGANISM: Arabidopsis thaliana

68 &lt;400&gt; SEQUENCE: 2

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73           20           25           30
75 Ser Asp Ser Ser Asn Gly Leu Leu Leu Ser Gly Ser Asp Asn Asn Ser
76           35           40           45
78 Pro Ser Asp Asp Val Gly Ala Pro Ala Asp Val Arg Asp Arg Ile Asp
79           50           55           60
81 Ser Val Val Asn Asp Asp Ala Gln Gly Thr Ala Asn Leu Ala Gly Asp
82   65           70           75           80
84 Asn Asn Gly Gly Gly Asp Asn Asn Gly Gly Arg Gly Gly Gly Glu
85           85           90           95
87 Gly Arg Gly Asn Ala Asp Ala Thr Phe Thr Tyr Arg Pro Ser Val Pro
88           100          105          110
90 Ala His Arg Arg Ala Arg Glu Ser Pro Leu Ser Ser Asp Ala Ile Phe
91           115          120          125
93 Lys Gln Ser His Ala Gly Leu Phe Asn Leu Cys Val Val Val Leu Ile
94           130          135          140
96 Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly Trp
97 145           150          155          160
99 Leu Ile Arg Thr Asp Phe Trp Phe Ser Ser Arg Ser Leu Arg Asp Trp
100           165          170          175
102 Pro Leu Phe Met Cys Trp Ile Ser Leu Ser Ile Phe Pro Leu Ala Ala
103           180          185          190
105 Phe Thr Val Glu Lys Leu Val Leu Gln Lys Tyr Ile Ser Glu Pro Val
106           195          200          205
108 Gly Ile Phe Leu His Ile Ile Ile Thr Met Thr Glu Val Leu Tyr Pro
109           210          215          220
111 Val Tyr Val Thr Leu Arg Cys Asp Ser Ala Phe Leu Ser Gly Val Thr
112 225           230          235          240
114 Leu Met Leu Leu Thr Cys Ile Val Trp Leu Lys Leu Val Ser Tyr Ala
115           245          250          255
117 His Thr Ser Tyr Asp Ile Arg Ser Leu Ala Asn Ala Ala Asp Lys Ala
118           260          265          270
120 Asn Pro Glu Val Ser Tyr Tyr Val Ser Leu Lys Ser Leu Ala Tyr Phe
121           275          280          285
123 Met Val Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Ser Ala

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124      290      295      300
126 Cys Ile Arg Lys Gly Trp Val Ala Arg Gln Phe Ala Lys Leu Val Ile
127 305      310      315      320
129 Phe Thr Gly Phe Met Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro Ile
130      325      330      335
132 Val Arg Asn Ser Lys His Pro Leu Lys Gly Asp Leu Leu Tyr Ala Ile
133      340      345      350
135 Glu Arg Val Leu Lys Leu Ser Val Pro Asn Leu Tyr Val Trp Leu Cys
136      355      360      365
138 Met Phe Tyr Cys Phe Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu
139      370      375      380
141 Leu Cys Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys
142 385      390      395      400
144 Ser Val Gly Asp Tyr Trp Arg Met Trp Asn Met Pro Val His Lys Trp
145      405      410      415
147 Met Val Arg His Ile Tyr Phe Pro Cys Leu Arg Ser Lys Ile Pro Lys
148      420      425      430
150 Thr Leu Ala Ile Ile Ile Ala Phe Leu Val Ser Ala Val Phe His Glu
151      435      440      445
153 Leu Cys Ile Ala Val Pro Cys Arg Leu Phe Lys Leu Trp Ala Phe Leu
154      450      455      460
156 Gly Ile Met Phe Gln Val Pro Leu Val Phe Ile Thr Asn Tyr Leu Gln
157 465      470      475      480
159 Glu Arg Phe Gly Ser Thr Val Gly Asn Met Ile Phe Trp Phe Ile Phe
160      485      490      495
162 Cys Ile Phe Gly Gln Pro Met Cys Val Leu Leu Tyr Tyr His Asp Leu
163      500      505      510
165 Met Asn Arg Lys Gly Ser Met Ser
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168 &lt;210&gt; SEQ ID NO: 3

169 &lt;211&gt; LENGTH: 1281

170 &lt;212&gt; TYPE: DNA

171 &lt;213&gt; ORGANISM: Zea mays

173 &lt;220&gt; FEATURE:

174 &lt;221&gt; NAME/KEY: unsure

175 &lt;222&gt; LOCATION: (356)

176 &lt;223&gt; OTHER INFORMATION: n = a, c, g, or t

178 &lt;220&gt; FEATURE:

179 &lt;221&gt; NAME/KEY: unsure

180 &lt;222&gt; LOCATION: (427)

181 &lt;223&gt; OTHER INFORMATION: n = a, c, g, or t

183 &lt;220&gt; FEATURE:

184 &lt;221&gt; NAME/KEY: unsure

185 &lt;222&gt; LOCATION: (1188)

186 &lt;223&gt; OTHER INFORMATION: n = a, c, g, or t

188 &lt;220&gt; FEATURE:

189 &lt;221&gt; NAME/KEY: unsure

190 &lt;222&gt; LOCATION: (1196)

191 &lt;223&gt; OTHER INFORMATION: n = a, c, g, or t

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TIME: 16:04:27

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Output Set: N:\CRF3\06042002\I856018B.raw

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204 <221> NAME/KEY: unsure
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214 <221> NAME/KEY: unsure
215 <222> LOCATION: (1248)
216 <223> OTHER INFORMATION: n = a, c, g, or t
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219 <221> NAME/KEY: unsure
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221 <223> OTHER INFORMATION: n = a, c, g, or t
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224 <221> NAME/KEY: unsure
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229 <221> NAME/KEY: unsure
230 <222> LOCATION: (1280)
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236 gctactacct gttttcacat cttttttaca acatttgaaa ttgtatatcc agtgctcgtg 180
237 attcttaagt gtgattctgc agttttatca ggctttgtgt tgatgtttat tgctgcatt 240
238 gtttggctga agcttgatc ttttgcacat acaaaccatg atataaggaa aactgatcac 300
W-> 239 aagcggcaag aagggttgata atgaactgac cgcggctggc atagataatt tacaanctcc 360
W-> 240 aactcttggg agtctaacat acttcaagat ggctccgaca ctctgttatc aagccaaagt 420
241 tatcctncga acaccttatg tttagaaaagg ttggctgggc cgtcaagtta ttctatactt 480
242 gatatttact ggtctccaag gattcattat tgagcaatac ataaatccta ttgttgtaaa 540
243 ctctcaacat ccattgatgg gaggattact gaatgctgta gagactgttt tgaagctctc 600
244 attaccaaatt gtctacctgt ggctttgcat gttttattgc cttttccatc tgtggttaaa 660
245 catacttgct gagattcttc gatttggatga ccgagaattc tacaaagact ggtggaatgc 720
246 aaagacaatt gatgagtact ggagaaaatg gaacatgcct gtgcataaat ggattgttcg 780
247 tcatatatat ttcccttgca tgcgaaatgg tatatcaaag gaagttgctg tttttatatc 840
248 gttctttgtt tctgctgtac ttcatgagtt atgtgttgcg gttccctgcc acatactcaa 900
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TIME: 16:04:27

Input Set : A:\BB1295 US PCT substitute sequence listing.txt

Output Set: N:\CRF3\06042002\I856018B.raw

250 caaaaataaa ttccagtgc caatgggttg caatatgatc ttttggtttt ttttctgcat 1020  
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 252 ggcaaaataa ccatctgtag atcttttttg gtttcatttc tccatcatgg aaactgaaac 1140  
 W- 253 ataactgtgc acacataaac agcatcgtgt ctcaattttt taaaaaanaa aagaananca 1200  
 W- 254 caaaaaaccc aggggggccc gtaccaatcc ccaaantatc gntnaccncc cacggcgnt 1260  
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 257 <210> SEQ ID NO: 4  
 258 <211> LENGTH: 361  
 259 <212> TYPE: PRT  
 260 <213> ORGANISM: Zea mays  
 262 <220> FEATURE:  
 263 <221> NAME/KEY: UNSURE  
 264 <222> LOCATION: (119)  
 265 <223> OTHER INFORMATION: Xaa = ANY AMINO ACID  
 267 <400> SEQUENCE: 4  
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 272 20 25 30  
 274 Phe Asn Asn Leu Val Ser Asp Pro Ala Thr Thr Cys Phe His Ile Leu  
 275 35 40 45  
 277 Phe Thr Thr Phe Glu Ile Val Tyr Pro Val Leu Val Ile Leu Lys Cys  
 278 50 55 60  
 280 Asp Ser Ala Val Leu Ser Gly Phe Val Leu Met Phe Ile Ala Cys Ile  
 281 65 70 75 80  
 283 Val Trp Leu Lys Leu Val Ser Phe Ala His Thr Asn His Asp Ile Gly  
 284 85 90 95  
 286 Lys Leu Ile Thr Ser Gly Lys Lys Val Asp Asn Glu Leu Thr Ala Ala  
 287 100 105 110  
 W- 289 Gly Ile Asp Asn Leu Gln Xaa Pro Thr Leu Gly Ser Leu Thr Tyr Phe  
 290 115 120 125  
 292 Lys Met Ala Pro Thr Leu Cys Tyr Gln Ala Lys Val Ile Leu Arg Thr  
 293 130 135 140  
 295 Pro Tyr Val Arg Lys Gly Trp Leu Val Arg Gln Val Ile Leu Tyr Leu  
 296 145 150 155 160  
 298 Ile Phe Thr Gly Leu Gln Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro  
 299 165 170 175  
 301 Ile Val Val Asn Ser Gln His Pro Leu Met Gly Gly Leu Leu Asn Ala  
 302 180 185 190  
 304 Val Glu Thr Val Leu Lys Leu Ser Leu Pro Asn Val Tyr Leu Trp Leu  
 305 195 200 205  
 307 Cys Met Phe Tyr Cys Leu Phe His Leu Trp Leu Asn Ile Leu Ala Glu  
 308 210 215 220  
 310 Ile Leu Arg Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala  
 311 225 230 235 240  
 313 Lys Thr Ile Asp Glu Tyr Trp Arg Lys Trp Asn Met Pro Val His Lys  
 314 245 250 255  
 316 Trp Ile Val Arg His Ile Tyr Phe Pro Cys Met Arg Asn Gly Ile Ser  
 317 260 265 270

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:7; N Pos. 1542,1543,1555,1556  
Seq#:9; N Pos. 491,577,806,893  
Seq#:10; Xaa Pos. 148,164,193,269,274  
Seq#:17; N Pos. 372,424,442,446,469  
Seq#:19; N Pos. 240,311,337,354,370,383,388,423,431,435,463,486,503,540,547  
Seq#:19; N Pos. 616,633,639  
Seq#:21; N Pos. 93